In the Claims:

Please cancel claim 1 without prejudice or disclaimer of the subject matter contained therein.

Please amend claims 2-11, 15-16, 23-25, and 27-30 as follows.

2. (Amended) The method according to claim 37, wherein the primer is a fragment of deoxyribonucleic or ribonucleic acid, an oligodeoxyribonucleotide, an oligoribonucleotide, or a copolymer of deoxyribonucleic acid and ribonucleic acid.

3. (Amended) The method according to claim 37, wherein the nucleic acid of interest is deoxyribonucleic acid, a ribonucleic acid, or a copolymer of deoxyribonucleic acid and ribonucleic acid.

4. (Amended) The method according to claim 37, wherein the target nucleotide is defined as any known base, which include wild-type or a known mutant base so long as the base is known and it is desired to know its variant.

5. (Amended) The method according to claim 37, wherein the terminator nucleotide is a dideoxyribonucleotide or an analogue thereof and the non-terminator nucleotide is a deoxyribonucleotide or a ribonucleotide or an analogue thereof.

6. (Amended) The method according to claim 37, wherein the terminator nucleotide is unlabeled.

7. (Amended) The method according to claim 37, wherein the terminator nucleotide is labeled with a detectable marker that is different from the marker on the non-terminators.

8. (Amended) The method according to claim 37, wherein in step (d), the duplex from step (c) is contacted with non-terminator nucleotides, wherein each non-terminators is labeled with the same or different detectable marker.

9. (Amended) The method according to claim 37, wherein said detectable marker comprises an enzyme, radioactive isotope, a fluorescent molecule, or a protein ligand.

10. (Amended) The method according to claim 38, wherein said detecting is carried out by mass spectrometry.

11. (Amended) The method according to claim 37, wherein said enzyme is template-dependent.

15. (Amended) The method according to claim 37, wherein the primer comprises one or more moieties that permit affinity separation of the primer from the unincorporated reagent and/or the nucleic acid of interest.

16. (Amended) The method according to claim 37, wherein the primer comprises one or more moieties that links the primer to a solid surface.

23. (Amended) The method according to claim 37, wherein the nucleic acid of interest has been synthesized enzymatically *in vivo*, *in vitro*, or synthesized non-enzymatically.

24. (Amended) The method according to claim 37, wherein the nucleic acid of interest is synthesized by polymerase chain reaction.

25. (Amended) The method according to claim 37, wherein the nucleic acid of interest comprises non-natural nucleotide analogs.

27. (Amended) The method according to claim 37, wherein the sample comprises genomic DNA from an organism, RNA transcripts thereof, or cDNA prepared from RNA transcripts thereof.

28. (Amended) The method according to claim 37, wherein the sample comprises extragenomic DNA from an organism, RNA transcripts thereof, or cDNA prepared from RNA transcripts thereof.

29. (Amended) The method according to claim 27, wherein the organism is a plant, microorganism, bacteria, or virus.

30. (Amended) The method according to claim 28, wherein the organism is a plant, microorganism, bacteria, or virus.

Please add the following new claims 37 and 38.

--37. A method for detecting or quantifying a target nucleic acid in a sample by detecting signal from a plurality of labeled nucleotides comprising:

(a) selecting a nucleic acid having a target nucleotide base at a predetermined position in a template of a nucleic acid of interest, wherein the target nucleotide base in original form is not immediately adjacent on its 3' side to an identical base;

(b) preparing an unlabeled primer complementary to a sequence immediately upstream of the target nucleotide base;

(c) treating a sample containing the nucleic acid of interest, if the nucleic acid is double-stranded, so as to obtain unpaired nucleotide bases spanning the specific position, or directly employing step (d) if the nucleic acid of interest is single-stranded;

(d) annealing the primer from (b) with the target nucleic acid from (c) under high stringency conditions to obtain a primer-nucleic acid duplex, wherein the target nucleotide base in the nucleic acid of interest is the first unpaired base immediately downstream of the 3' end of the primer;

(e) mixing the primer-nucleic acid duplex from (d) with a primer extension reaction reagent comprising: (i) three types of non-terminator nucleotides that are not complementarily matched to the target nucleotide, wherein at least one type of the non-terminator nucleotide is labeled with a detectable marker; and optionally (ii) one type of terminator nucleotide that is complementarily matched to the target nucleotide, wherein the terminator nucleotide is not labeled;

(f) performing the primer extension reaction by enzymatic or chemical means, wherein the incorporation of said non-terminator nucleotide and optionally, the terminator nucleotide, to the primer extension depends upon the identity of the unpaired nucleotide base in the nucleic acid template, and wherein when the target nucleotide is changed to any other type of nucleotide, a plurality of non-terminator nucleotides labeled with said detectable marker are sequence-dependently incorporated into the primer extension; and

(g) determining the presence of the mutated nucleotide base at the predetermined position in the nucleic acid of interest by detecting the presence of detectable signal of the non-terminator nucleotides extended from the primer. --

--38. A method for detecting or quantifying a target nucleic acid in a sample comprising:

(a) selecting a nucleic acid having a target nucleotide base at a predetermined position in a template of a nucleic acid of interest, wherein the target nucleotide base in original form is not immediately adjacent on its 3' side to an identical base;

(b) preparing a primer complementary to a sequence immediately upstream of the target nucleotide base;

(c) treating a sample containing the nucleic acid of interest, if the nucleic acid is double-stranded, so as to obtain unpaired nucleotide bases spanning the specific position, or directly employing step (d) if the nucleic acid of interest is single-stranded;

(d) annealing the primer from (b) with the target nucleic acid from (c) under high stringency conditions to obtain a primer-nucleic acid duplex, wherein the target nucleotide

base in the nucleic acid of interest is the first unpaired base immediately downstream of the 3' end of the primer;

(e) mixing the primer-nucleic acid duplex from (d) with a primer extension reaction reagent comprising three types of non-terminator nucleotides that are not complementarily matched to the target nucleotide;

(f) performing the primer extension reaction by enzymatic or chemical means, wherein the incorporation of said non-terminator nucleotide into the primer extension depends upon the identity of the unpaired nucleotide base in the nucleic acid template, wherein when the target nucleotide base is changed to another type of nucleotide, a plurality of non-terminator nucleotides are sequence-dependently incorporated into the primer extension; and

(g) determining the presence of the mutated nucleotide base at the predetermined position in the nucleic acid of interest by detecting the length of the primer extended strand, wherein if the primer extended strand is longer than the primer the presence of the mutated nucleotide base is indicated. --

b6 cont.

REMARKS

Claims 2-38 are pending in the application. The amendment to the specification at page 9 has been made to remove unnecessary material, thereby further clarifying the specification. Bases for the newly added claims 37 and 38 can be found at, *inter alia*, pages 4 and 18 in the in the present specification, in which the primer strand is extended with a plurality of labeled nucleotides. Additional support for the newly added claim 38 can be found at, *inter alia*, page 14 in the present specification, in which the extended primer strand may be identified through conventional methods, such mass spectroscopy when the nucleotides are not labeled with a